
Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Mon Jun 11 13:25:27 EDT 2007

Reviewer Comments:

seq Id 6:

Missing amino acid numbering, they non-aligned 645,650,655

Please delete text appearing after seq id 21.

Validated By CRFValidator v 1.0.2

Application No: 10813507 Version No: 2.0

Input Set:

Output Set:

Started: 2007-05-25 16:08:39.424 **Finished:** 2007-05-25 16:08:48.098

Elapsed: 0 hr(s) 0 min(s) 8 sec(s) 674 ms

Total Warnings: 30
Total Errors: 681

No. of SeqIDs Defined: 21
Actual SeqID Count: 21

Err	or code	Error Description
W	112	Upper case found in data; Found at position(0) SeqId(6)
W	112	Upper case found in data; Found at position(3) SeqId(6)
W	112	Upper case found in data; Found at position(6) SeqId(6)
W	112	Upper case found in data; Found at position(9) SeqId(6)
W	112	Upper case found in data; Found at position(12) SeqId(6)
E	342	'n' position not defined found at POS: 15 SEQID(6)
W	112	Upper case found in data; Found at position(15) SeqId(6)
W	112	Upper case found in data; Found at position(18) SeqId(6)
W	112	Upper case found in data; Found at position(21) SeqId(6)
W	112	Upper case found in data; Found at position(24) SeqId(6)
W	112	Upper case found in data; Found at position(27) SeqId(6)
W	112	Upper case found in data; Found at position(30) SeqId(6)
W	112	Upper case found in data; Found at position(33) SeqId(6)
W	112	Upper case found in data; Found at position(36) SeqId(6)
W	112	Upper case found in data; Found at position(39) SeqId(6)
W	112	Upper case found in data; Found at position(42) SeqId(6)
W	112	Upper case found in data; Found at position(45) SeqId(6)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (644)
E	323	Invalid/missing amino acid numbering SEQID (6)at Protein (645)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (649)

Input Set:

Output Set:

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Error code		Error Description
E	323	Invalid/missing amino acid numbering SEQID (6)at Protein (650)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (654)
E	323	Invalid/missing amino acid numbering SEQID (6)at Protein (655)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (659)
E	323	Invalid/missing amino acid numbering SEQID (6)at Protein (660)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (664)
E	323	Invalid/missing amino acid numbering SEQID (6)at Protein (665)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (669)
E	323	Invalid/missing amino acid numbering SEQID (6)at Protein (670)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (674)
E	323	Invalid/missing amino acid numbering SEQID (6)at Protein (675)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (679)
E	323	Invalid/missing amino acid numbering SEQID (6)at Protein (680)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (684)
E	323	Invalid/missing amino acid numbering SEQID (6)at Protein (685)
E	323	Invalid/missing amino acid numbering SEQID (6) POS (689)
E	323	Invalid/missing amino acid numbering SEQID (6) at Protein (690) This error has occured more than 20 times, will not be displayed
E	331	Count of Protein differs from the <211> tag Input: 2351 Calculated: 2335 SEQID(6)
W	213	Artificial or Unknown found in <213> in SEQ ID (14)
W	213	Artificial or Unknown found in <213> in SEQ ID (15)
W	213	Artificial or Unknown found in <213> in SEQ ID (16)

Input Set:

Output Set:

Started: 2007-05-25 16:08:39.424 **Finished:** 2007-05-25 16:08:48.098

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Total Warnings: 30

Total Errors: 681

No. of SeqIDs Defined: 21

Actual SeqID Count: 21

Err	or code	Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (17)
W	213	Artificial or Unknown found in <213> in SEQ ID (18)
W	213	Artificial or Unknown found in <213> in SEQ ID (19)
W	213	Artificial or Unknown found in <213> in SEQ ID (20)
W	213	Artificial or Unknown found in <213> in SEQ ID (21)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (21)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (21)
W	112	Upper case found in data; Found at position(0) SeqId(21)
W	112	Upper case found in data; Found at position(1) SeqId(21)
W	112	Upper case found in data; Found at position(2) SeqId(21)
W	112	Upper case found in data; Found at position(14) SeqId(21) This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Lollar, John S. <120> Nucleic Acid and Amino Acid Sequences encoding High-Level Expressor Factor VIII Polypeptides and Methods of Use <130> 007157/ 276516 <140> 10813507 <141> 2004-03-30 <150> PCT/US02/33403 <151> 2002-10-07 <150> 60/327,388 <151> 2001-10-05 <160> 21 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 6402 <212> DNA <213> Sus scrofa <220> <221> gene <222> (1)...(6399) <223> Factor VIII-- Full Length <221> CDS <222> (1)...(6399) <400> 1 atg cag cta gag ctc tcc acc tgt gtc ttt ctg tgt ctc ttg cca ctc 48 Met Gln Leu Glu Leu Ser Thr Cys Val Phe Leu Cys Leu Leu Pro Leu 5 ggc ttt agt gcc atc agg aga tac tac ctg ggc gca gtg gaa ctg tcc 96 Gly Phe Ser Ala Ile Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser tgg gac tac cgg caa agt gaa ctc ctc cgt gag ctg cac gtg gac acc Trp Asp Tyr Arg Gln Ser Glu Leu Leu Arg Glu Leu His Val Asp Thr 35 40 45 aga ttt cct gct aca gcg cca gga gct ctt ccg ttg ggc ccg tca gtc 192 Arg Phe Pro Ala Thr Ala Pro Gly Ala Leu Pro Leu Gly Pro Ser Val 50 55 ctg tac aaa aag act gtg ttc gta gag ttc acg gat caa ctt ttc agc 240 Leu Tyr Lys Lys Thr Val Phe Val Glu Phe Thr Asp Gln Leu Phe Ser 65 70 75 80

_	-			agg Arg 85				_		_	_					288
_	-		-	tac Tyr	_	_		-	_		_	_		_	_	336
			-	agt Ser			-	-		-						384
	-		-	gaa Glu			-			_				_	_	432
-	-		-	ctt Leu				-				-		_	_	480
_		-		ggt Gly 165			-		_			_				528
		_		cac His		_	_			_	_		_			576
		-	_	ctg Leu	-	-	-	_		_	-		_	_		624
	_		-	cac His	-		-				-	-		-	_	672
		_		cac His		-	-		-					-	_	720
_		-		gcc Ala 245		-	_		_	_			-		2 2	768
	-			tct Ser	_			_			_					816
-				gtg Val			_			-	_	-				864
			-	ggc Gly		_							_	_	_	912

	_	gag Glu		_							-	_			_	960
_	-	ctt Leu		_			_		_							1008
		ggc Gly			-		-	_	_	_	_	_	-			1056
	_	ctg Leu 355				-	_	_		_	_		_	_		1104
_		gac Asp	_	_	_	_					_		_	_		1152
		ttt Phe				_	_	_	-	_	_					1200
		cac His				-				_		-		_		1248
	-	ccc Pro	-		-	-	-	_			_			_		1296
_		cct Pro 435	_	_								-	_		_	1344
_		acg Thr	-	-			_		-		_		_		_	1392
		atc Ile	_							_	-		_			1440
_		ata Ile		_				_	-							1488
		atc Ile		_	-	-	_	_				_				1536
		aaa Lys 515		-		-	_			_						1584
aag	tat	aaa	tgg	aca	gtg	act	gtg	gaa	gat	ggg	cca	acc	aag	tcc	gat	1632

Lys	Tyr 530	Lys	Trp	Thr	Val	Thr 535	Val	Glu	Asp	Gly	Pro 540	Thr	Lys	Ser	Asp	
		-	-		-			_	-		att Ile					1680
-	_	-	-								atc Ile				_	1728
	-	-		_			_	_	_		gac Asp	_	_		_	1776
	_			-		-				_	tgg Trp			-		1824
		_	_					_	-		tta Leu 620	_		_	_	1872
				-				_		-	atc Ile				-	1920
	-	_	_	_	_	_	-	-	_		gag Glu		-			1968
			_	_		_	_	_	_		ctc Leu		_			2016
								_	-		gaa Glu	-				2064
											tca Ser 700					2112
			-			-				-	ttg Leu			_		2160
_		_		_	_			_	_	_	agg Arg	_			_	2208
		-				-	-				ttc Phe	_	_	-		2256
_		-		_		_	_		_	_	aat Asn		_			2304

755 760 765

_		_		_							agt Ser 780		_	_	_	2352
			-	_	_				_		caa Gln	_	_	_	_	2400
	_	_				_	223	_	_		ttg Leu		_			2448
_								-			gaa Glu	_				2496
_	-	_					_	_	_	_	ggc Gly	_	-			2544
_		-	_		_			_			agt Ser 860	_	_	_	_	2592
								-	_		ctt Leu	-			_	2640
	_			-			_		_		aca Thr				_	2688
_	_		, ,			_					tta Leu					2736
_	_	-				_				_	att Ile	_		, ,		2784
							_		_		ttg Leu 940		_			2832
945	_		-	_		_		_		-	tca Ser				_	2880
945 gac	ggg	His ata	Glu	Ser	Ser 950 aag	Leu	Gly	Glu	Asn cat	Val 955 gga		Pro gct	Val tca	Glu	Ser 960 acc	2928

aaq qca cqa qt	tac tta aaa	act aat aga	aaq att cac a	it gat gac	3024
Lys Ala Arg Va.		_	-		
gca gct tta tt	a act gag aat	agg gca tct	gca acg ttt a	g gac aaa	3072
Ala Ala Leu Lei 1010	ı Thr Glu Asn 101	_	Ala Thr Phe Mo	et Asp Lys	
aat act aca gc				333	3120
Asn Thr Thr Al	a Ser Gly Leu 1030	Asn His Val	Ser Asn Trp I	le Lys Gly 1040	
ccc ctt ggc aa					3168
Pro Leu Gly Ly	1045	105		1055	
ctt ctg aca tc				J J	3216
10	_	1065		070	
ggg cag ggg ag Gly Gln Gly Are					3264
1075	, ,	1080	1085		
ggc aaa gag ato Gly Lys Glu Me	-				3312
1090	109		1100		
tcg gct gat gte Ser Ala Asp Va				-	3360
1105	1110	-	1115	1120	
cgg gaa gag ato Arg Glu Glu Me		Ī	-		3408
	1125	113	0	1135	
ttg cct cag gto Leu Pro Gln Va			_	2 2	3456
11	10	1145	1	150	
att ttt cac cad Ile Phe His Gl				333 333	3504
1155		1160	1165		
tca cat gcg ccc Ser His Ala Pre			_		3552
1170	117	5	1180		
gag aga gca gad Glu Arg Ala Gl				,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	3600
1185	1190		1195	1200	
gca ccc ttg gad Ala Pro Leu Gl	ı Ala Pro Gly	Asn Arg Thr	Gly Pro Gly P	ro Arg Ser	3648
	1205	121	0	1215	

gcg g Ala V			-	Arg	-	_	_	-	Leu		_		-	Leu	-	3696
cta g Leu G	3lu	_	Ile	_		_		Gly		_	_		Āla			3744
acc c Thr A		Trp		-	-	-	Pro					Ala		_		3792
aac c Asn I 1265						Leu		_	-	_	Ala					3840
aag a Lys I		_	_	_	Gly			Ī	_	Gly		_			Gly	3888
aag c Lys I	_		_	Ala	-				Ala		_		-	Ala		3936
ggc a	-ys	-	Glu					Val	-	-			Glu	-	_	3984
ttg c Leu F		Gln			-		Val		_	-		Gly	_			4032
cag g Gln G 1345	_			_	_	Lys					Val		_			4080
gta a Val A		-			Arg				-	Leu	-			_	Met	4128
ccc a				Glu				_	Ser			_		Āla		4176
agg a	acg	aaa	gac	atc	atc	agt	tta	ccc	ctg	gac	cgt	cac	gaa	agc	aat	4224